



Table III

Oligonucleotide Primers Used for RT-PCR Analysis and DNA Sequencing

| Primer | SEQ ID NO: | Sequence | Position | PCR Product (bp) | Peptide Sequences confirmed |
|--------|------------|---------------------------|-----------|------------------|-----------------------------|
| BAB1F | 5 | TCAATATAATCTGGCGAATGCAAT | 3-26 | | |
| HSP2R | 7 | AGTTCCGAATGGGCAGGTCAGCTC | 397-420 | 418 | 3 |
| BAB3F | 26 | ATGAGGAAGCTCGGGTTAAAG | 1452-1472 | | |
| BAB4R | 29 | GATGTAGCCATTGTTTGTGTCCTCA | 1769-1792 | 341 | 2 |
| HSP2F | 33 | GAGCTGACCTGCCCATTCGGAAC | 397-420 | | |
| HSP3R | 35 | CTTTAACCCGAGCTTCCTCAT | 1452-1472 | 1076 | 4 |
| BAB6F | 30 | AGACGCCAAATGTGTGACCTCCA | 3078-3101 | | |
| BAB7R | 31 | GAATAGGCCAGCACTTCCGTCAGG | 3510-3533 | 456 | 2 |
| BAB1F | 5 | TCAATATAATCTGGCGAATGCAAT | 3-26 | | |
| BAB10R | 32 | GGTGAGGCAGTTGGCGCTGGTATG | 851-874 | 872 | 3 |
| HSP2F | 33 | GAGCTGACCTGCCCATTCGGAAC | 397-420 | | |
| BAB10R | 32 | GGTGAGGCAGTTGGCGCTGGTATG | 851-874 | 478 | 3 |
| BAB10F | 34 | CATACCAGCGCCAACTGCCTCACC | 851-874 | | |
| HSP3R | 35 | CTTTAACCCGAGCTTCCTCAT | 1452-1472 | 622 | 3 |
| BAB9F | 36 | CAAGTACGGCATCCACTGTGACCA | 697-720 | | |
| HSP3R | 35 | CTTTAACCCGAGCTTCCTCAT | 1452-1472 | 776 | 3 |

Other Primers used for RT-PCR and sequencing.

| Name | SEQ ID NO: | Sequence | Position |
|------|------------|--------------------------|-----------|
| 5F | 37 | GGCTACTTCGGGCGAGACTGTCAG | 2386-2409 |
| 5R | 38 | CTGACAGTCTCGCCCGAAGTAGCC | 2386-2409 |
| 8F | 39 | TTGTACTCTTCAGCTGGCACC | 4406-4426 |
| 8R | 6 | GGTGCCAGCTGAAGAGTACAA | 4406-4426 |

Table IV

Summary of Amino Acid Sequences Derived From Peptides of the
Purified Human 190 kDa HARE Protein

The human HARE proteins were immuno-affinity-purified from human spleen, subjected to SDS-PAGE and the 190 kDa protein band was excised and analyzed for internal peptide sequence following trypsin digestion. The amino acid sequences of these ten tryptic peptides were highly homologous or identical to the sequences of the rat 175 kDa HARE, reported herein above, and seven of these (not in bold face) were identical to regions within a human hypothetical protein of unknown expression and unknown function under GenBank accession number BAB15793. HARE peptides in boldface were not in the ORF for BAB15793.

| Peptide Designation | Amino Acid Sequences | Start-End Residue | SEQ ID NO: |
|-------------------------------|-------------------------|-------------------|------------|
| PR 1822 | XSKPK | 758-761 | 40 |
| PR 1823 | LTFDK | 1054-1058 | 41 |
| PR 1825-1 st | GSIQELPK | 440-448 | 42 |
| PR 1825-2 nd | GTLFVPQNSGLGE | 1198-1210 | 43 |
| PR 1826 | DLVGPGPFTVFAPLSAAFDEEAR | 466-488 | 44 |
| PR 1869-1st | ELTSPFGTK | 133-141 | 45 |
| PR 1869-2 nd | MPQVLR | 498-503 | 46 |
| PR 1870 | SPLGQYK | 1047-1053 | 47 |
| PR 1871-1st | VLEIQK | 107-112 | 48 |
| PR 1872 | VIHGLGK | 100-106 | 49 |

Table V

Molecular Mass Mapping of Peptides Derived From the

Human 190 kDa HARE Protein

THE MOLECULAR MASSES OF SEVEN PEPTIDES DERIVED FROM TRYPTIC DIGESTION OF THE PURIFIED HUMAN 190 KDA HARE PROTEIN WERE DETERMINED BY MALDI-TOF MASS SPECTROMETRY AT THE LOUISIANA STATE UNIVERSITY PROTEIN CHEMISTRY FACILITY CORRESPONDED WITH PERFECT IDENTITY TO DEDUCED SEQUENCES WITHIN A PREDICTED HUMAN PROTEIN OF UNKNOWN FUNCTION (ACCESSION NUMBER BAB15793). THE MONOISOTOPIC PEPTIDE MASSES WERE SEARCHED AGAINST ENTRIES IN THE DATABASE, USING PEPTIDESEARCH SOFTWARE FROM THE EMBL PROTEIN AND PEPTIDE GROUP. IDENTICAL MASSES ARE ASSIGNED IN THIS SEARCH IF THE DIFFERENCE BETWEEN THE OBSERVED AND PREDICTED (CALCULATED) MASSES FOR A PEPTIDE IS < 0.2 DA. THE CORRESPONDING STARTING AND ENDING RESIDUES FOR EACH PEPTIDE WITHIN THE DEDUCED PROTEIN SEQUENCE IS SHOWN. THE N-TERMINAL R OR K RESIDUES IN PARENTHESES INDICATE THE DEDUCED RESIDUE IN THE PROTEIN AND CONFIRM THAT TRYPSIN DIGESTION OCCURRED ON THE C-TERMINAL SIDE OF THOSE AMINO ACIDS AS EXPECTED.

| Measured Mass (Da) | Calculated Mass (Da) | Mass Difference (Da) | Start-End Residues | Sequence in Deduced Human | SEQ ID NO: |
|--------------------|----------------------|----------------------|--------------------|---------------------------|------------|
| 599.273 | 599.294 | -0.021 | 796-800 | (K)GYFGR | 50 |
| 671.384 | 671.399 | -0.015 | 656-660 | (K)FHVIR | 51 |
| 792.621 | 792.426 | 0.195 | 1047-1053 | (R)SPLGQYK | 52 |
| 1034.621 | 1034.552 | 0.068 | 440-448 | (R)GSIYQELPK | 53 |
| 1061.781 | 1061.584 | 0.196 | 677-686 | (K)TLQGSELSVK | 54 |
| 1624.051 | 1623.886 | 0.165 | 1047-1060 | (R)SPLGQYKLTFDKAR | 55 |
| 1092.771 | 1092.588 | 0.183 | 495-503 | (K)YGLMPQVLR | 56 |



In the Sequence Listing:

Please delete the Sequence Listing submitted on pages 139-207 of the Specification and substitute therefore the substitute Sequence Listing filed herewith under 37 CFR 1.825. The Sequence Listing filed with the application on April 25, 2001 did not contain a SEQ ID NO:37, and therefore the substitute Sequence Listing submitted herewith has been renumbered so that SEQ ID NOs:38-57 are now SEQ ID NOs:37-56. The Specification has been amended herein above to also reflect such renumbering of the SEQ ID NOs. In addition, the substitute Sequence Listing has been reformatted to fully comply with 37 CFR 1.821-1.823. The substitute Sequence Listing contains no new matter.

Also submitted herewith is a substitute copy of the Computer Readable Form of the substitute Sequence Listing under 37 CFR 1.825 which fully complies with the requirements of 37 CFR 1.821-1.824. The Computer Readable Form contains all previously submitted data with the above requested amendments incorporated therein. The copy of the Sequence Listing in Computer Readable Form is the same as the substitute copy of the Sequence Listing filed herewith.